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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/700,293

DATE: 12/26/2000
 TIME: 13:14:21

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\12262000\I700293.raw

ENTERED

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4 <110> APPLICANT: SmithKline Beecham Biologicals
5   Ruelle, Jean-Louis
7 <120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides
8   from Neisseria Meningitidis
11 <130> FILE REFERENCE: BM15321
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/700,293
C--> 13 <141> CURRENT FILING DATE: 2000-11-13
13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03255
14 <151> PRIOR FILING DATE: 1999-05-07
16 <150> PRIOR APPLICATION NUMBER: GB 9810276.7
17 <151> PRIOR FILING DATE: 1998-05-13
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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24 <211> LENGTH: 1785
25 <212> TYPE: DNA
26 <213> ORGANISM: Bacteria
28 <400> SEQUENCE: 1
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30 gagctcacac gcaaccacac caaacgcgcc tcgcgaaccg tggcgaccgc cgtattggcg      120
31 acactgttgt ttgcaacggc tcaaggcagc actaccgatg acgacgattt atatttagaa      180
32 cccgtacaac gcaactgctgt cgtgtttgagc ttccgtttccg ataaagaagg caccggagaa      240
33 aaagaagtta cagaagattc aaattgggga gtatatltcg acaagaaagg agtactaaca      300
34 gccggaacaa tcacccctcaa agccggcgac aacctgaaaa tcaaacaaaa caccaatgaa      360
35 aacaccaatg ccagtatgctt cacctactcg ctgaaaaaag acctcacaga tctgaccagt      420
36 gttggaactg aaaaattatc gtttagcgca aacagcaata aagtcacat cacaagcgac      480
37 accaaaggct tgaatttcgc gaaaaaaacg gctgagacca accggcgacac caccggttcat      540
38 ctgaacggta tcggttcgac tttagaccgat acgctgctga alaccggayc gaccacaaac      600
39 gtaaccaacy acaacgttac cgtgacgag aaaaaacgtg cggcaagcgt taaagacgta      660
40 ttaaacgcag gctggaacat taaaggcggt aaaaccggtc caacagcttc cgataacggt      720
41 gatitcgtcc gcacttacga cacagtcgag ttcttgagcg cagatacga aacaacgact      780
42 gttaatgttg aaagcaaaag caacggcaag agaaccgaag ttaaaatcgg tgcgaagact      840
43 tctgttatca aagaaaaagu cggtaagttg gttactggta aagacaaagg cgagaatgat      900
44 tctttacacg acaaaaggcg aggcttagtg actgcaaaaag aagtgtatga tgcagttaac      960
45 aaggctggtt ggagaatgaa aacaacaacc gctaatygtc aaacaggtca agctgacaag      1020
46 tttagaaacc ttacatcagg cacaalgtg acctttgcta gtggtaaagg tacaactgcg      1080
47 actgtaagta angatgatca aggcaacatc actgtlatgt atgatgtaaa tgtcggcgat      1140
48 gccctaaacg tcaatcagct gcaaaacagc ggttggaatt tggattccaa agcgggttga      1200
49 ggtttcttcg qcaaaagtcac cagcggcaat qtttcgcccga gcaagggaag gatggatgaa      1260
50 accgltcaaca ttaatgccgg caacaacatc gagatlaacc gcaacggcaa aaatatcgac      1320
51 atcgccactt cgtatgacccc gcaattttcc agcgtttccg tcggcgccgg ggcggatgcg      1380
52 cccactltta gcgtggatga cgaagggcgg ttgaatgtcg gcagcaagga tgcacaaaa      1440
53 cccgtccgca ttaccaatgt cgcgccgggc gttaaagagg gggatgttac aaacgtcgca      1500
54 caacttaaa gcggtggcga aaacttgaac aaccacatcg acaatgtlga cggcaacgcg      1560
55 cgtgcgggca tcgcccaagc gatttcaacc gcaggtcttg ttcaggcgta tctgcccgcc      1620
56 aagagtatga tggcgatcgg cggcggcaat tctcgccggc aagcgggtta tgcacatcgg      1680
57 tactcaagca ttcccgacgg cggaaattgg attatcaaa gcaacggcttc cggcaattcg      1740

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58 cgcggccatc tccgtgcttc cgcactctgc ggttatcagt ggtaa          1785
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 594
62 <212> TYPE: PRT
63 <213> ORGANISM: Bacteria
65 <400> SEQUENCE: 2
66 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
67 1 5 10 15
68 Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
69 20 25 30
70 Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
71 35 40 45
72 Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
73 50 55 60
74 Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu
75 65 70 75 80
76 Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
77 85 90 95
78 Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
79 100 105 110
80 Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr
81 115 120 125
82 Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu
83 130 135 140
84 Lys Leu Ser Phe Ser Ala Asn Ser Asn Lys Val Asn Ile Thr Ser Asp
85 145 150 155 160
86 Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Glu Thr Asn Gly Asp
87 165 170 175
88 Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
89 180 185 190
90 Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
91 195 200 205
92 Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
93 210 215 220
94 Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val
95 225 230 235 240
96 Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
97 245 250 255
98 Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr
99 260 265 270
100 Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
101 275 280 285
102 Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Asp Ser Ser Thr Asp
103 290 295 300
104 Lys Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn
105 305 310 315 320
106 Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
107 325 330 335
108 Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe

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109          340          345          350
110 Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
111          355          360          365
112 Asn Ile Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
113          370          375          380
114 Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala
115 385          390          395          400
116 Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
117          405          410          415
118 Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
119          420          425          430
120 Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
121          435          440          445
122 Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
123          450          455          460
124 Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
125 465          470          475          480
126 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
127          485          490          495
128 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
129          500          505          510
130 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
131          515          520          525
132 Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
133          530          535          540
134 Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
135 545          550          555          560
136 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
137          565          570          575
138 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
139          580          585          590
140 Gln Trp

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143 <210> SEQ ID NO: 3

144 <211> LENGTH: 1776

145 <212> TYPE: DNA

146 <213> ORGANISM: Bacteria

148 <400> SEQUENCE: 3

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149 atgaacaaaa tataccgcac catattggaat agtgccctca atgcctgggt cgcgcgtatcc 60
150 gagctcacac gcaaccacac caaacgcgcc tccgcaaccg tgaagaccgc cgtattggcg 120
151 acaactgttgt ttgcaaccgt tcaggcaagt gctaacaalg aagagcaaga agaagattta 180
152 tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccga taaagaaggc 240
153 acgggagaaa aagaaaaagt agaagaaaat tcagattggg cagtatatit caacgagaa 300
154 gtagtactaa cagccagaga aatcacccctc aaagccggcg acaacctgaa aatcaaacaa 360
155 aacggcacaa acctcaccta ctgcctgaaa aaagacctca cagatctgac cagtgttggg 420
156 actgaaaaat tatcgttttg cgcacaacggc aataaaagtc acatcacaa 480
157 ggcttgaatt ttgcgaaaga aacggctggg acgaacggcg acaccacggt tcacctgaac 540
158 ggtathtggtt cgactttgac cgatcacgctg ctgaataccg gagcgaccac aaacgtaacc 600
159 aacgacaacg ttaccgatga cgagaaaaaa cgtgcggcaa gcgtlaaaga cgtattaaac 660
160 gcaggctgga acattaaagg cyttaaaccc ggtacaacag ctcccgataa cyttgatttc 720

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161 gtcgcgaactt acgacacagt cgaagtcttg agcgagata cgaatacaac gactttaa 780
162 gtygaagca aagacaacgg caagaaaacc gaagtlaaa tcggtgcga gacttctgtt 840
163 attaaagaa aaqacggtaa gttggttact ggtaaagaca aagcgagaa tggttcttct 900
164 acagacgaag cgaagggctt agtgactgca aaagaagtga ttgatgcagt aaacaaggct 960
165 ggttgagaa tgaatacaac aaccgctaatt ggtcaaacag gtcaagctga caagtctgaa 1020
166 accgttacat caggcacaaa tgtacacctt gctagtgtga aaggtaaac tgcgactgta 1080
167 agtaaaqatg atcaagqcaa catcactgtt atgtatgatg taaatgtcga cgaatcccta 1140
168 aacgtcaatc agctgcaaaa cagcgggttg aatttggtt ccaagcggt tgcaggttct 1200
169 tcgggcaaa gtcacagcgg caatgtttcg ccgagcaagg gaaagatgga tgaaccgtc 1260
170 aacattaatg ccggcaacaa catcgagatt acccgcaacg gtaaaaaal cgaatcgcc 1320
171 acttcgatga ccccgcaatt ttcacagctt tcgctcggcg cggggcgga tgcgccact 1380
172 ttgagcgtg atggggacgc attgaatgtc ggcagcaaga aggacaaca acccgctcgc 1440
173 attaccaatg tcgccccggg cgttaaagag qgggatgta caaacgtcg acaactaaa 1500
174 ggcgtggcg aaaaactgaa caaccgcac gacaaatgtg acggcaacgc gctgcggcg 1560
175 atcgcccaag cgaattgcaac cgcaggtctg gttcagggc atttgcccg caagagtatg 1620
176 atggcgtatg cggcgccgac ttatcgccgc gaaacgggt acgcacatcg ctactccagt 1680
177 atttcgacg ggggaaattg gattatcaaa ggcacggctt ccggcaatc ggcggccat 1740
178 ttccgtgctt ccgcactctg cggttatcag tggtaa 1776
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 591
182 <212> TYPE: PRT
183 <213> ORGANISM: Bacteria
185 <400> SEQUENCE: 4
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187 1 5 10 15
188 Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
189 20 25 30
190 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
191 35 40 45
192 Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
193 50 55 60
194 Val Glu Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
195 65 70 75 80
196 Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
197 85 90 95
198 Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
199 100 105 110
200 Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser
201 115 120 125
202 Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
203 130 135 140
204 Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
205 145 150 155 160
206 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
207 165 170 175
208 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
209 180 185 190
210 Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
211 195 200 205

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212 Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
213      210      215      220
214 Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
215 225      230      235      240
216 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
217      245      250      255
218 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
219      260      265      270
220 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
221      275      280      285
222 Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
223      290      295      300
224 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
225 305      310      315      320
226 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Glu Ala
227      325      330      335
228 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
229      340      345      350
230 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
231      355      360      365
232 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
233      370      375      380
234 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
235 385      390      395      400
236 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
237      405      410      415
238 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
239      420      425      430
240 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
241      435      440      445
242 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
243      450      455      460
244 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
245 465      470      475      480
246 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
247      485      490      495
248 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
249      500      505      510
250 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
251      515      520      525
252 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
253      530      535      540
254 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
255 545      550      555      560
256 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
257      565      570      575
258 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
259      580      585      590
261 <210> SEQ ID NO: 5

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VERIFICATION SUMMARY DATE: 12/26/2000
PATENT APPLICATION: US/09/700,293 TIME: 13:14:22

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\12262000\1700293.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date